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09/762,045	09/17/2001	Andrea Reindl	817/000006	7926

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WASHINGTON, DC 20036

EXAMINER

KALLIS, RUSSELL

ART UNIT PAPER NUMBER

1638

DATE MAILED: 10/06/2004

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary

Application No.

09/762,045

Applicant(s)

REINDL ET AL.

Examiner

Russell Kallis

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-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

- 1) ☒ Responsive to communication(s) filed on 19 July 2004.
- 2a) ☐ This action is **FINAL**. 2b) ☒ This action is non-final.
- 3) ☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

- 4) ☒ Claim(s) 1-22 is/are pending in the application.
- 4a) Of the above claim(s) 5-8, 11, 12, 15, 16 and 20-22 is/are withdrawn from consideration.
- 5) ☐ Claim(s) _____ is/are allowed.
- 6) ☒ Claim(s) 1-4, 9, 10, 13, 14 and 17-19 is/are rejected.
- 7) ☐ Claim(s) _____ is/are objected to.
- 8) ☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

- 9) ☐ The specification is objected to by the Examiner.
- 10) ☒ The drawing(s) filed on 01 February 2001 is/are: a) ☒ accepted or b) ☐ objected to by the Examiner.
Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).
Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).
- 11) ☒ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

- 12) ☒ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
- a) ☒ All b) ☐ Some * c) ☐ None of:
- ☐ Certified copies of the priority documents have been received.
 - ☐ Certified copies of the priority documents have been received in Application No. _____.
 - ☒ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

- 1) ☒ Notice of References Cited (PTO-892)
- 2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
- 3) ☒ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08)
Paper No(s)/Mail Date 7/30/01.
- 4) ☐ Interview Summary (PTO-413)
Paper No(s)/Mail Date. _____
- 5) ☐ Notice of Informal Patent Application (PTO-152)
- 6) ☒ Other: attached sequence reports.

DETAILED ACTION

Claims 1-22 are pending. Claims 5-8, 11-12, 15-16 and 20-22 are withdrawn. Claims 1-4, 9-10, 13-14 and 17-19 are examined.

Election/Restrictions

Applicant's election without traverse of Group I, Claims 1-4, 9-10, 13-14 and 17-19; and SEQ ID NO: 1 in the reply filed on July 19, 2004 is acknowledged.

Oath/Declaration

The oath or declaration is defective. A new oath or declaration in compliance with 37 CFR 1.67(a) identifying this application by application number and filing date is required. See MPEP §§ 602.01 and 602.02.

The oath or declaration is defective because: Non-initialed and/or non-dated alterations have been made to the oath or declaration. See 37 CFR 1.52(c).

Specification

The use of the trademark Gene Clean and PCR-Script has been noted in this application. It should be capitalized wherever it appears and be accompanied by the generic terminology.

Although the use of trademarks is permissible in patent applications, the proprietary nature of the marks should be respected and every effort made to prevent their use in any manner which might adversely affect their validity as trademarks.

Claim Rejections - 35 USC § 112

The following is a quotation of the first paragraph of 35 U.S.C. 112:

The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

Claims 1-4 and 9-10 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

Applicant broadly claims the use of DNA sequences coding for a 1-deoxy-D-xylulose-5-phosphate synthase (DOXS) and a p-hydroxyphenylpyruvate dioxygenase (HPPD); the use of DNA sequences that hybridize to SEQ ID NO: 1 or SEQ ID NO: 5 and encode a DOXS or a HPPD for producing plants with increased content of tocopherols, vitamin K, chlorophylls, and/or carotenoids; and a process for producing plants with increased tocopherol, vitamin K, chlorophyll and/or carotenoids which express either a 1-deoxy-D-xylulose-5-phosphate synthase (DOXS) or both a DOXS and a p-hydroxyphenylpyruvate dioxygenase (HPPD) or DNA sequences that hybridize to SEQ ID NO: 1 and encode a DOXS, or hybridize to SEQ ID NO: 1 and SEQ ID NO: 5 and encode a DOXS or a HPPD.

Applicant describes DOXS encoding polynucleotides from *Arabidopsis* of SEQ ID NO 1, from *E. coli* of SEQ ID NO: 3, and incorporates through reference the DOXS encoding polynucleotide from peppermint (page 6 specification); and the HPPD sequence of SEQ ID NO: 5 from *S. avermitilis*.

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Applicant does not describe DNA sequences encoding DOXS or HPPD that hybridize to SEQ ID NO: 1 or SEQ ID NO: 5 or any other DOXS or HPPD encoding DNA sequence other than those encoding DOXS from *Arabidopsis* of SEQ ID NO 1, from *E. coli* of SEQ ID NO: 3, and the DMA sequence encoding DOXS from peppermint; or any other HPPD encoding DNA sequence other than SEQ ID NO: 5.

The Federal Circuit has recently clarified the application of the written description requirement to inventions in the field of biotechnology. The court stated that, “A description of a genus of cDNAs may be achieved by means of a recitation of a representative number of cDNAs, defined by nucleotide sequence, falling within the scope of the genus or of a recitation of structural features common to members of the genus, which features constitute a substantial portion of the genus.” *See University of California v. Eli Lilly and Co.*, 119 F.3d 1559; 43 USPQ2d 1398, 1406 (Fed. Cir. 1997).

Applicants fail to describe a representative number of DOXS or HPPD encoding polynucleotides. Applicants only describe DOXS of SEQ ID NO: 1 from *Arabidopsis* and SEQ ID NO: 3 from *E. coli*, incorporate through reference the DOXS sequence from peppermint; and the HPPD sequence of SEQ ID NO: 5 from *S. avermitilis*. Furthermore, Applicants fail to describe structural features common to members of the claimed genus of DOXS and HPPD encoding sequences. Hence, Applicants fail to meet either prong of the two-prong test set forth by *Eli Lilly*. Furthermore, given the lack of description of the necessary elements essential for DOXS or HPPD activity, it remains unclear what features identify a DOXS or HPPD encoding DNA sequence. Since the genus of DNA sequences encoding a protein having DOXS activity or

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HPPD activity has not been described by specific structural features, the specification fails to provide an adequate written description to support the breadth of the claims.

Sequences that hybridize with SEQ ID NO: 1 or SEQ ID NO: 5 encompass naturally occurring allelic variants, mutants of DOXS or HPPD genes, as well as sequences encoding proteins having no known DOXS or HPPD activity, of which Applicant is not in possession. Accordingly, the specification fails to provide an adequate written description to support the genus of DNA sequence encoding proteins having DOXS or HPPD activity encompassed by the hybridization language as set forth in the claims. (See Written Description guidelines published in Federal Register/Vol. 66, No.4/Friday, January 5, 2001/Notices: p.1099-1111).

Claims 1-4 and 9-10 are rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for the use of SEQ ID NO: 1; and SEQ ID NO: 1 and SEQ ID NO: 5 together for producing plants that have increased tocopherol, vitamin K, chlorophyll, and/or carotenoids; and a method for producing plants with increased tocopherol, vitamin K, chlorophyll, and/or carotenoids which express SEQ ID NO: 1 or both SEQ ID NO: 1 and 5, does not reasonably provide enablement for the use of any sequence that hybridizes to SEQ ID NO: 1 or SEQ ID NO: 5 and encodes a DOXS or HPPD or any DOXS or HPPD encoding polynucleotide; or a method of increasing tocopherol, vitamin K, chlorophyll, and/or carotenoids in a plant which expresses any sequence that hybridizes to SEQ ID NO: 1 or SEQ ID NO: 5 and encodes a DOXS or HPPD or any plant transformed with an expression cassette which expresses any DOXS or DOXS and HPPD other than SEQ ID NO: 1 or SEQ ID NO: 5. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make or use the invention commensurate in scope with these claims.

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The claimed invention is not supported by an enabling disclosure taking into account the *Wands* factors. *In re Wands*, 858/F.2d 731, 8 USPQ2d 1400 (Fed. Cir. 1988). *In re Wands* lists a number of factors for determining whether or not undue experimentation would be required by one skilled in the art to make and/or use the invention. These factors are: the quantity of experimentation necessary, the amount of direction or guidance presented, the presence or absence of working examples of the invention, the nature of the invention, the state of the prior art, the relative skill of those in the art, the predictability or unpredictability of the art, and the breadth of the claim.

Applicant broadly claims the use of DNA sequences coding for a 1-deoxy-D-xylulose-5-phosphate synthase (DOXS) and a p-hydroxyphenylpyruvate dioxygenase (HPPD); the use of DNA sequences that hybridize to SEQ ID NO: 1 or SEQ ID NO: 5 and encode a DOXS or a HPPD for producing plants with increased content of tocopherols, vitamin K, chlorophylls, and/or carotenoids; and a process for producing plants with increased tocopherol, vitamin K, chlorophyll and/or carotenoids which express either a 1-deoxy-D-xylulose-5-phosphate synthase (DOXS) or both a DOXS and a p-hydroxyphenylpyruvate dioxygenase (HPPD) or DNA sequences that hybridize to SEQ ID NO: 1 and encode a DOXS, or hybridize to SEQ ID NO: 1 and SEQ ID NO: 5 and encode a DOXS or a HPPD.

Applicant teaches an expression construct comprising SEQ ID NO: 1 (Example 1 page 29), a transformation method (Example 1 page 29), and increased levels of total chlorophylls and total carotenoids in *Arabidopsis* transformed with a sense expression construct comprising SEQ ID NO: 1 (Example 6 page 33); an expression construct comprising SEQ ID NO: 3 and SEQ ID NO: 5 (Example 11 pages 37-39), a transformation method (Example 13 pages 39-40), and

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increased α -tocopherol levels in *Brassica napus* transformed with SEQ ID NO: 3 expressing an *E. coli* DOXS homolog and SEQ ID NO: 5 expressing an HPPD from *S. avermitilis* (Examples 14 page 41).

Applicant does not teach the isolation of any previously unknown DNA sequences that encode either a DOXS or HPPD from any source. The specification fails to provide guidance for the isolation or synthesis of other polynucleotides that encode a DOXS or HPPD encompassed by the claims. Applicants fail to teach which amino acids can be altered and still produce a protein with the same functions as the proteins encoded by SEQ ID NO: 1 or SEQ ID NO: 5.

The state of the art for isolating DNA fragments using highly stringent hybridization conditions, does not always select for DNA fragments whose contiguous nucleotide sequence is the same or nearly the same as the probe and is therefore unpredictable. Fourgoux-Nicol et al (1999, *Plant Molecular Biology* Vol. 40; pp. 857-872) teach the isolation of a 674bp fragment using a 497bp probe incorporating stringent hybridization conditions comprising three consecutive 30 minute rinses in 2X, 1X and 0.1X SSC with 0.1% SDS at 65°C (page 859, left column, 2nd paragraph). Fourgoux-Nicol et al also teach that the probe and isolated DNA fragment exhibited a number of sequence differences comprising a 99bp insertion within the probe and a single nucleotide gap, while the DNA fragment contained 2 single nucleotide gaps and together the fragments contained 27 nucleotide mismatches. Taking into account the insertions, gaps and mismatches, the longest stretch of contiguous nucleotides to which the probe could hybridize consisted of 93bp of DNA (page 862, Figure 2).

The state of the art for the isolation of orthologous DNA sequences from other species introduces an element of unpredictability because finding homologous regions that would

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adequately enable either PCR amplification or southern hybridization when the amplification or hybridization target is unknown is a limiting factor and would entail using either degenerate primers or probes with limited sequence identity. Thus the screen for orthologous sequences would isolate many genes other than those of interest. The inherent unpredictability in isolation of a homologous sequence encoding the same protein activity is illustrated in an example where a small number of changes to the coding region for a strict desaturase resulted in an enzyme with a hydroxylase activity showing that a small number of changes to the coding region of a desaturase could account for the functional divergence seen across a range of enzymes involved in fatty acid metabolism (Broun P. *et al.* Science Vol. 282; 13 November 1998, pp. 1315-1317; Abstract lines 4-6 and p. 1317 column 1, lines 37-56).

Given the lack of guidance in the instant specification, undue trial and error experimentation would be required for one of ordinary skill in the art to screen through a multitude of non-exemplified sequences, either by using fragments of SEQ ID NO: 1 and 5 as probes, and isolating or amplifying fragments, subcloning the fragments, producing expression vectors and transforming plants therewith, in order to identify those polynucleotides that when expressed have DOXS or HPPD activity and produce plants with increased content of tocopherols, vitamin K, chlorophyll, and/or carotenoids.

Therefore, given the breadth of the claims; the lack of guidance and working examples; the unpredictability in the art; and the state-of-the-art as discussed above, undue experimentation would be required to practice the claimed invention, and therefore the invention is not enabled throughout the broad scope of the claims.

The following is a quotation of the second paragraph of 35 U.S.C. 112:

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The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

Claims 1-4 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

Claims 1-4 provide for the use of DNA sequences, but, since the claim does not set forth any steps involved in the method/process, it is unclear what method/process applicant is intending to encompass. A claim is indefinite where it merely recites a use without any active, positive steps delimiting how this use is actually practiced.

Claims 1-4 are rejected under 35 U.S.C. 101 because the claimed recitation of a use, without setting forth any steps involved in the process, results in an improper definition of a process, i.e., results in a claim which is not a proper process claim under 35 U.S.C. 101. See for example *Ex parte Dunki*, 153 USPQ 678 (Bd.App. 1967) and *Clinical Products, Ltd. v. Brenner*, 255 F. Supp. 131, 149 USPQ 475 (D.D.C. 1966).

Claim Rejections - 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless –

(b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

Claims 1-2, 9-10, 13-14 and 17-18 are rejected under 35 U.S.C. 102(b) as being anticipated by Mandel M. *et al.* Plant Journal, 1996; Vol. 9, No. 5, pp. 649-658 in light of Estevez J. *et al.* Plant Physiology, September 2000; Vol. 124, pp. 95-103 and the attached sequence report.

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Mandel teaches CLA1, a gene isolated using a fragment of a mutant CLA1 gene of an albino tDNA insertion mutant of *Arabidopsis* (*cla1*) that was deficient in chlorophyll and carotenoids. Estevez teaches that CLA1 encodes a 1-deoxyxylulose-5-phosphate synthase of SEQ ID NO: 1 (see Abstract, lines 1-4, and the first paragraph of the Discussion section on page 99; and attached sequence report). Mandel further teaches complementation of the *cla1* *Arabidopsis* mutant via *Agrobacterium*-mediated transformation (pages 651-652) that resulted in dramatic increases in the levels of chylorophyll and carotenoids when compared to the levels of chylorophyll and carotenoids found in the *cla1* mutant (page 652 in Table 1) and thus teaches a process for producing plants with increased tocopherol, vitamin K, chlorophyll and/or carotenoid contents, a process for transforming a plant and transformed plant thereof, and a use for SEQ ID NO: 1. Thus, the reference teaches all the limitations of Claims 1-2, 9-10, 13-14 and 17-18.

Claim Rejections - 35 USC § 103

The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

(a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negated by the manner in which the invention was made.

Claims 1-4, 9-10, 13-14 and 17-19 are rejected under 35 U.S.C. 103(a) as being unpatentable over Mandel M. *et al.* Plant Journal, 1996; Vol. 9, No. 5, pp. 649-658 in view of Dellapenna D. WO 97/27285 published July 31, 1997; and in further view of Estevez J. *et al.* Plant Physiology, September 2000; Vol. 124, pp. 95-103.

Mandel teaches CLA1, a gene isolated using a fragment of a mutant CLA1 gene of an albino tDNA insertion mutant of *Arabidopsis* (*cla1*) that was deficient in chlorophyll and

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carotenoids. Mandel further teaches complementation of the *cla1 Arabidopsis* mutant via *Agrobacterium*-mediated transformation (pages 651-652) that resulted in dramatic increases in the levels of chlorophyll and carotenoids when compared to the levels of chlorophyll and carotenoids found in the *cla1* mutant (page 652 in Table 1) and thus teaches a process for producing plants with increased tocopherol, vitamin K, chlorophyll and/or carotenoid contents, a process for transforming a plant and transformed plant thereof, and a use for SEQ ID NO: 1.

Dellapenna teaches a cDNA clone from *Arabidopsis* encoding HPPD and a method of producing a transgenic plant using the *Arabidopsis* HPPD clone to increase the production of vitamin E (tocopherols), plastoquinones and carotenoids (page 26, lines 10-18); and incorporates through reference the HPPD from *S. avermitilis* as taught by Denoya C. D. on page 24 lines 14-21 (SEQ ID NO: 5 of the instant claims, see attached sequence report).

Estevez teaches that CLA1 encodes the 1-deoxyxylulose-5-phosphate synthase of SEQ ID NO: 1 of the instant claims (see Abstract, lines 1-4, and the first paragraph of the Discussion section on page 99; and attached sequence report).

It would have been obvious at the time of invention to modify the invention of Mandel to include a HPPD encoding polynucleotide as taught by Dellapenna. One of skill in the art would have been motivated by the knowledge common in the art that isoprenoid products (i.e. tocopherols, vitamin K, chlorophyll, and carotenoids) are important in the production of plant pigments as taught by Mandel, and because the genes encoding DOXS and HPPD synthesize the precursors to tocopherols, vitamin K, chlorophyll, and carotenoids, are recognized in the art for their value for genetically engineering plants to increase the levels of those plant isoprenoid derived compounds also taught by Dellapenna; and that DOXS and HPPD genes were available

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in the art as taught by Applicant's specification and by Dellapenna; that one would have had a reasonable expectation of success of transforming plants with DOXS and HPPD genes and success in selecting for transformed plants having increased levels of tocopherols, vitamin K, chlorophyll, and/or carotenoids given the success of Mandel; wherein combining two transgenes into one plant and wherein choosing soybean, canola, barley, oats, wheat, oilseed rape, corn or sunflower as a target species is an obvious design step given the lack of criticality.

All claims are rejected.

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Any inquiry concerning this communication or earlier communications from the examiner should be directed to Russell Kallis whose telephone number is (571) 272-0798. The examiner can normally be reached on M-F 8:30-5.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Amy Nelson can be reached on (571) 272-0804. The fax phone number for the organization where this application or proceeding is assigned is 703-872-9306.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see <http://pair-direct.uspto.gov>. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

A handwritten signature in cursive script that reads "Russell Kallis".

Russell Kallis Ph.D.
September 30, 2004

attached sequence report

acid dioxygenase-like protein that directs the production of homogenetic acid and an ochronotic pigment in Escherichia coli J. Bacteriol. 176 (17), 5312-5319 (1994)

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MEDLINE
PUBMED
REFERENCE
2 (bases 1 to 1469)
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TITLE
Direct Submission
JOURNAL
Submitted (06-JUL-1994) Claudio D. Denoya, Bioprocess Research, Pfizer Inc., Eastern Point Road, Groton, CT 06340, USA
FEATURES
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ORIGIN

Query Match 100.0%; Score 1469; DB 1; Length 1469;
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QY 1201 CGTACTACGACACCTTCGGGAGTGGGTGGCGACACCCCGCTCCCGTCCGACACCTGC 1260
DB 1201 CGTACTACGACACCTTCGGGAGTGGGTGGCGACACCCCGCTCCCGTCCGACACCTGC 1260
QY 1261 GCGAGCTGAAGATCCTCGCGACCGCGACGAGGACGGCTATCTGCTCCAGATCTTACCA 1320
DB 1261 GCGAGCTGAAGATCCTCGCGACCGCGACGAGGACGGCTATCTGCTCCAGATCTTACCA 1320
QY 1321 AGCGGTTCAGGACCGCGCGGCTTCCTTCAGATCATCGAACGCCCGCTCGATGG 1380
DB 1321 AGCGGTTCAGGACCGCGCGGCTTCCTTCAGATCATCGAACGCCCGCTCGATGG 1380
QY 1381 GATTTCGCAAGGCAACTTCAAGCCCTTTCGAGCGGATCGAGCGGAGCAGGAGAAGC 1440
DB 1381 GATTTCGCAAGGCAACTTCAAGCCCTTTCGAGCGGATCGAGCGGAGCAGGAGAAGC 1440
QY 1441 GGGGCACTGTAGCGCGCGCGCGCGG 1469
DB 1441 GGGGCACTGTAGCGCGCGCGCGCGG 1469

RESULT 2
BD249658
LOCUS
DEFINITION
DNA sequence coding for a 1-deoxy-d-xylulose-5-phosphate synthase and the overproduction thereof in plants.
ACCESSION
BD249658
VERSION
BD249658.1 GI:33059428
KEYWORDS
JP 2002525034-A/3.

BD249658 1469 bp DNA linear PAT 17-JUL-2003
DNA sequence coding for a 1-deoxy-d-xylulose-5-phosphate synthase and the overproduction thereof in plants.
BD249658
BD249658.1 GI:33059428
JP 2002525034-A/3.

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 15, 2004, 11:58:35 ; Search time 5704.3 Seconds
(without alignments)
11161.918 Million cell updates/sec

Title: US-09-762-045A-5

Perfect score: 1469

Sequence: 1 gatattcgagcgccgcggg.....tgtagcgcgcgccgcggg 1469

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb.ba.*

2: gb.bhg.*

3: gb.in.*

4: gb.om.*

5: gb.ov.*

6: gb.pat.*

7: gb.ph.*

8: gb.pl.*

9: gb.pr.*

10: gb.ro.*

11: gb.sts.*

12: gb.sy.*

13: gb.un.*

14: gb.vi.*

15: em.ba.*

16: em.fun.*

17: em.hum.*

18: em.in.*

19: em.mu.*

20: em.om.*

21: em.or.*

22: em.ov.*

23: em.pat.*

24: em.ph.*

25: em.pl.*

26: em.ro.*

27: em.sts.*

28: em.un.*

29: em.vi.*

30: em.htg.hum.*

31: em.htg.inv.*

32: em.htg.other.*

33: em.htg.mus.*

34: em.htg.pln.*

35: em.htg.rod.*

36: em.htg.mam.*

37: em.htg.vrt.*

38: em.sv.*

39: em.hngo.hum.*

40: em.hngo.mus.*

41: em.hngo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1469	100.0	1469	1	SAU11864	U11864 Streptomyces
2	1469	100.0	1469	6	BD249658	BD249658 DNA seque
3	1445	98.4	4994	1	AB070935	AB070935 Streptomy
4	1445	98.4	300425	1	AP005041	AP005041 Streptomy
5	1126	76.7	313800	1	SC093911	SC093911 Streptomy
6	640.2	43.6	1159	6	AX085149	AX085149 Streptomy
7	640.2	43.6	1159	6	AX417724	AX417724 Sequence
8	590.4	40.2	2298	6	AX219431	AX219431 Sequence
9	585.6	39.9	1206	6	AR219432	AR219432 Sequence
10	307.6	20.9	106111	8	NCE23G1	NCE23G1
11	270.4	18.4	276800	1	SC093911	SC093911 Streptomy
12	263.8	18.0	1421	9	BC024287	BC024287 Homo sapi
13	263.8	18.0	1421	9	HSPPD	HSPPD
14	263.8	18.0	1896	9	AK057510	AK057510 Homo sapi
15	263.8	18.0	88421	6	AX417445	AX417445 Sequence
16	263.2	17.9	2850	8	AF038152	AF038152 Mycosphae
17	261.6	17.8	1460	8	AF325533	AF325533 Magnapor
18	252.6	17.2	1432	10	BC013343	BC013343 Mus muscu
19	251.6	17.1	1507	3	AY047523	AY047523 Drosophi
20	249.4	17.0	1399	10	MUS4HD	MUS4HD
21	245.2	16.7	1176	10	MMFPROT	MMFPROT
22	243	16.5	1140	6	AX467159	AX467159 Sequence
23	236.6	16.1	55972	1	AF386507	AF386507 Streptomy
24	233.4	15.9	1361	10	AF082834	AF082834 Rattus no
25	233.4	15.9	89153	1	NSP561198	NSP561198 Actinoma
26	229.2	15.6	1333	10	RATANTF	RATANTF
27	221	15.0	204050	1	AL646073	AL646073 Ralstonia
28	220.8	15.0	69301	1	STU82965	STU82965 Streptomyce
29	209.2	14.2	37941	1	AOPCZA361	AOPCZA361
30	206.2	14.0	10895	1	AE004521	AE004521 Pseudomon
31	204.6	13.9	56917	1	AME16952	AME16952 Amycolatops
32	198.8	13.5	1260	4	PIGHPD	PIGHPD
33	197.6	13.5	301846	1	AE016913	AE016913 Chromobac
34	193.8	13.2	10369	1	AE005921	AE005921 Caulobact
35	191.4	13.0	34805	1	EX640434	EX640434 Bordetell
36	191.4	13.0	348074	1	EX640449	EX640449 Bordetell
37	184.4	12.6	290029	2	AE017024	AE017024 Bacillus
38	184.2	12.5	95597	2	AC014022	AC014022 Drosophi
39	184.2	12.5	194790	3	AC009840	AC009840 Drosophi
40	184.2	12.5	301136	3	AE003591	AE003591 Drosophi
41	183.4	12.5	348134	1	EX640420	EX640420 Bordetell
42	183.2	12.5	307343	1	AE016998	AE016998 Bacillus
43	175.4	11.9	1250	5	AY398361	AY398361 Danio rer
44	175.4	11.9	1818	5	BC046075	BC046075 Danio rer
45	171.4	11.7	10246	1	AE012141	AE012141 Xanthomon

ALIGNMENTS

RESULT 1	SAU11864	1469 bp	DNA	linear	BCT 08-OCT-1994
LOCUS	Streptomyces avermitilis ATCC 31272	4-hydroxyphenylpyruvate acid			
DEFINITION	Streptomyces avermitilis ATCC 31272	4-hydroxyphenylpyruvate acid			
ACCESSION	U11864	dicboxgenase gene, complete cds.			
VERSION	U11864.1	GI:538272			
KEYWORDS	Streptomyces avermitilis				
SOURCE	Streptomyces avermitilis				
ORGANISM	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;				
REFERENCE	Streptomycineae; Streptomycetaceae; Streptomycetes.				
AUTHORS	1. (bases 1 to 1469)				
TITLE	Denoya, C.D., Skinner, D.D. and Morgenstern, M.R.				
	A Streptomyces avermitilis gene encoding a 4-hydroxyphenylpyruvic				

attached sequence report

QY	1741	AGAATTTTAAAGGAAGGAGAGAGTTGGTTGTTGGGTTATGGCTCAGCAGTTCCAGAGC	1800
Db	1741	AGAATTTTAAAGGAAGGAGAGAGTTGGTTGTTGGGTTATGGCTCAGCAGTTCCAGAGC	1800
QY	1801	TGTTTAGGAGCGGCTGTAAATGCTCGAAGAACCGGATTAACGTAACCTGATCGCGATGCA	1860
Db	1801	TGTTTAGGAGCGGCTGTAAATGCTCGAAGAACCGGATTAACGTAACCTGATCGCGATGCA	1860
QY	1861	CGGTTTTCGAAGCCATTGGACCGTGCTCTCAITTCGACGCTTAGCTAGTCGACGAGTT	1920
Db	1861	CGGTTTTCGAAGCCATTGGACCGTGCTCTCAITTCGACGCTTAGCTAGTCGACGAGTT	1920
QY	1921	CTGATCAGCGTTGAAGAAGGTTCCATTGGAGGTTTTGGCTCGCAGCTTGTTCAGTTCTT	1980
Db	1921	CTGATCAGCGTTGAAGAAGGTTCCATTGGAGGTTTTGGCTCGCAGCTTGTTCAGTTCTT	1980
QY	1981	GCTCTCGATGCTCTCTTTGATGGCAAACTCAAGTGGAGACCAATGGTACTGCTGATCGA	2040
Db	1981	GCTCTCGATGCTCTCTTTGATGGCAAACTCAAGTGGAGACCAATGGTACTGCTGATCGA	2040
QY	2041	TACATTGATCAGCGTGCAACAGCTGATCAACTAGCTGAAGCTGACCTCATGCCATCTCAC	2100
Db	2041	TACATTGATCAGCGTGCAACAGCTGATCAACTAGCTGAAGCTGACCTCATGCCATCTCAC	2100
QY	2101	ATCGCAGCAACCGCACCTTAACCTTAATCGGTGCACCAAGGAGAGCTGTTTGAGAGTAA	2160
Db	2101	ATCGCAGCAACCGCACCTTAACCTTAATCGGTGCACCAAGGAGAGCTGTTTGAGAGTAA	2160
QY	2161	GAATCTGTTGGCTAAAAACATATGATACAACTCTAAATGCAACCAAGGTTTCTTCT	2220
Db	2161	GAATCTGTTGGCTAAAAACATATGATACAACTCTAAATGCAACCAAGGTTTCTTCT	2220
QY	2221	AAGTACTGATCAGAAATCCCGCCGAGAGTCCCTTTGGCAACAGCTATATATTACTA	2280
Db	2221	AAGTACTGATCAGAAATCCCGCCGAGAGTCCCTTTGGCAACAGCTATATATTACTA	2280
QY	2281	AGATTGTGAAGAGAAAGCAAGGCTGTGCAAGATTAGTATTATAGATAAACC	2340
Db	2281	AGATTGTGAAGAGAAAGCAAGGCTGTGCAAGATTAGTATTATAGATAAACC	2340
QY	2341	TGGTATTGTTTGTGTAATTTTAGAATGTGATGAGATCGTGTGACCAATACTAACAT	2400
Db	2341	TGGTATTGTTTGTGTAATTTTAGAATGTGATGAGATCGTGTGACCAATACTAACAT	2400
QY	2401	CTTGTAATAATCAATTAATCTCTTGTGATCTTCAATAAGCTTGAGTGACAAAAAAA	2458
Db	2401	CTTGTAATAATCAATTAATCTCTTGTGATCTTCAATAAGCTTGAGTGACAAAAAAA	2458
RESULT 2			
LOCUS	ATU27099	2458 bp	mRNA linear
DEFINITION	Arabidopsis thaliana DEF (CLA1)	mRNA, complete cds.	
ACCESSION	U27099		
VERSION	U27099.1	GI:1399260	
KEYWORDS			
SOURCE	Arabidopsis thaliana (thale cress)		
ORGANISM	Arabidopsis thaliana		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosids; eucosids II; Brassicales; Brassicaceae; Arabidopsids.		
REFERENCE	1 (bases 1 to 2458)		
AUTHORS	Mandel, A., Rocha-Sosa, M., Herrera-Estrella, L., Feldmann, K.A. and Leon, P.		
TITLE	Direct Submission		
JOURNAL	Submitted (12-MAY-1995) Patricia Leon-Wejia, Plant Molecular Biology, Instituto de Biociencia, UNAM, Apdo. Postal 510-3, Cuernavaca, MOR 62271, Mexico		
REFERENCE	2 (bases 1 to 2458)		
AUTHORS	Mandel, M.A., Feldmann, K.A., Herrera-Estrella, L., Rocha-Sosa, M. and Leon, P.		
TITLE	CLA1, a novel gene required for chloroplast development, is highly conserved in evolution		

QY 421 CTTTGGGATGTTGGTCATCAGTCTTATACCTCATAAAGATCTTCTTCTGAGAGAGGAAAG 480
DB 421 CTTTGGGATGTTGGTCATCAGTCTTATCTCTCATAAAGATCTTCTTCTGAGAGAGGAAAG 480
QY 481 ATGCCCTACAAATGAGGCAAAACCAATGCTCTCTCTGTTTCCACCAACGAGGAGAGAGTCAA 540
DB 481 ATGCCCTACAAATGAGGCAAAACCAATGCTCTCTCTGTTTCCACCAACGAGGAGAGAGTCAA 540
QY 541 CATGATGCTTTGGTACTGGACACAGCTCAACCAATATCTGCTGTTTGGATGAGGCG 600
DB 541 CATGATGCTTTGGTACTGGACACAGCTCAACCAATATCTGCTGTTTGGATGAGGCG 600
QY 601 GTAGGAGGGAATTTGAGGGGAGAGACACAAATGTTGTTGCTGATTTGGTACTGGTGG 660
DB 601 GTAGGAGGGAATTTGAGGGGAGAGACACAAATGTTGTTGCTGATTTGGTACTGGTGG 660
QY 661 ATGACGGCAGGACAGGCTTATGAAGCCATGAACCAACGCGCGGATCTAGACTCTGATATG 720
DB 661 ATGACGGCAGGACAGGCTTATGAAGCCATGAACCAACGCGCGGATCTAGACTCTGATATG 720
QY 721 ATTGTGATCTTAAATGACAAACGCAAGTCTCTATTACCTAGCTACTTTGGATGGACCA 780
DB 721 ATTGTGATCTTAAATGACAAACGCAAGTCTCTATTACCTAGCTACTTTGGATGGACCA 780
QY 781 AGTCCACCTGTTGGTGCATTGAGCAGTCTCTTAGTCCGTTACAGTCTAAACCGGCTCTC 840
DB 781 AGTCCACCTGTTGGTGCATTGAGCAGTCTCTTAGTCCGTTACAGTCTAAACCGGCTCTC 840
QY 841 AGAGAGTTGAGAGAGTCCAAAGGGTATGACAAAGCAATAGGCGGACCAATGATCAG 900
DB 841 AGAGAGTTGAGAGAGTCCAAAGGGTATGACAAAGCAATAGGCGGACCAATGATCAG 900
QY 901 TTGGCGGCTAAGGTAGATGCTATGCTCGAGGAATGATAAGCGGTACTGGATCGTCACTG 960
DB 901 TTGGCGGCTAAGGTAGATGCTATGCTCGAGGAATGATAAGCGGTACTGGATCGTCACTG 960
QY 961 TTGTAAGAACTCGTCTTTACTATATTTGTCAGTTGATGGGCAACAATAGATGATTTG 1020
DB 961 TTGTAAGAACTCGTCTTTACTATATTTGTCAGTTGATGGGCAACAATAGATGATTTG 1020
QY 1021 GTAGCCATTCTTAAAGAACTTAAGATACCAAGACCAAGGACCTGTACTTATTATCATGTG 1080
DB 1021 GTAGCCATTCTTAAAGAACTTAAGATACCAAGACCAAGGACCTGTACTTATTATCATGTG 1080
QY 1081 GTGACGGAGAAAGTGGTGGTTATCTTACGCGGAGAGCTGTATGACAAATACCATGGT 1140
DB 1081 GTGACGGAGAAAGTGGTGGTTATCTTACGCGGAGAGCTGTATGACAAATACCATGGT 1140
QY 1141 GTTGTGAATTTGATCCGACACGGGTAGACAGTTCAAACTACTTAATGAGACTCAATCT 1200
DB 1141 GTTGTGAATTTGATCCGACACGGGTAGACAGTTCAAACTACTTAATGAGACTCAATCT 1200
QY 1201 TACACAACTTACTTTGCGGAGGCAATPAGTCGAGAGCAGAGGTAGACAAAGATGTGGTT 1260
DB 1201 TACACAACTTACTTTGCGGAGGCAATPAGTCGAGAGCAGAGGTAGACAAAGATGTGGTT 1260
QY 1261 GCGATTCATGACGACCTAGGAGGTGAACCGGGTTAAATCTCTTTCAAGTCGCTTCCCA 1320
DB 1261 GCGATTCATGACGACCTAGGAGGTGAACCGGGTTAAATCTCTTTCAAGTCGCTTCCCA 1320
QY 1321 ACAAGATGTTTCGATGAGGAATAGCGGAAACAACGCAAGTACTTTTCTCGCGGTTTA 1380
DB 1321 ACAAGATGTTTCGATGAGGAATAGCGGAAACAACGCAAGTACTTTTCTCGCGGTTTA 1380
QY 1381 GCCTGTGAGGCGCTTAAACCCCTCTCTGTGCAATCTATTCCTTTTATGAGCGTCTTAT 1440
DB 1381 GCCTGTGAGGCGCTTAAACCCCTCTCTGTGCAATCTATTCCTTTTATGAGCGTCTTAT 1440
QY 1441 GACCAGGTTGTCATGATGTTGATTTGCAAAAATACCGTGGAGATTTCCAAATGATAGA 1500
DB 1441 GACCAGGTTGTCATGATGTTGATTTGCAAAAATACCGTGGAGATTTCCAAATGATAGA 1500

RESULT 3
BT002340
LOCUS
DEFINITION Arabidopsis thaliana clone C104921 putative DEF (CLAL) protein
ACCESSION BT002340
VERSION BT002340.1
KEYWORDS FLI_CDNA.

BT002340 2185 bp mRNA linear PLN 15-DEC-2002
Arabidopsis thaliana clone C104921 putative DEF (CLAL) protein
(At4g15560) mRNA, complete cds.
BT002340
BT002340.1 GI:26983841
FLI_CDNA.

QY 1501 GTTGGACTCGTTGGAGCTGATGGTCCGACACATTTGGAGCTTTGATGTGATTAATG 1560
DB 1501 GTTGGACTCGTTGGAGCTGATGGTCCGACACATTTGGAGCTTTGATGTGATTAATG 1560
QY 1561 GCTTGTCTTCCCTAAACATGATAGTGGCTCCATCAGATGAGAGCAGATCTCTTTAAACATG 1620
DB 1561 GCTTGTCTTCCCTAAACATGATAGTGGCTCCATCAGATGAGAGCAGATCTCTTTAAACATG 1620
QY 1621 GTTGCACACTGCTGTTGCGATTGATGATCGTCTCTTCTTGTCTTCCGTTACCTTAGAGGTAAAC 1680
DB 1621 GTTGCACACTGCTGTTGCGATTGATGATCGTCTCTTCTTGTCTTCCGTTACCTTAGAGGTAAAC 1680
QY 1681 GGTATTGGAGTTGCACTTACCTCCGGAACAAAGGTGTCCTCAATTGAGATTGGGAAAGGT 1740
DB 1681 GGTATTGGAGTTGCACTTACCTCCGGAACAAAGGTGTCCTCAATTGAGATTGGGAAAGGT 1740
QY 1741 AGAATTTTAAAGGAAGAGAGAGAGTGGCTTGTGTTGGGTATATGGCTCAGCAGTTCAGAGC 1800
DB 1741 AGAATTTTAAAGGAAGAGAGAGAGTGGCTTGTGTTGGGTATATGGCTCAGCAGTTCAGAGC 1800
QY 1801 TGTATTAGGAGCGGCTGTAATGCTCGAAGAACCGGATTAACGCTAACTGTAGCGATGCA 1860
DB 1801 TGTATTAGGAGCGGCTGTAATGCTCGAAGAACCGGATTAACGCTAACTGTAGCGATGCA 1860
QY 1861 CGGTTTTCGAAGCATTGGACCGTCTCTCATTTGCGAGCTTAGCTAAAGTCGCACGAGGTT 1920
DB 1861 CGGTTTTCGAAGCATTGGACCGTCTCTCATTTGCGAGCTTAGCTAAAGTCGCACGAGGTT 1920
QY 1921 CTGATCACCGTTGAAGAGGTTCCATTGGAGGTTTGGCTCGCAGCTTGTTCAGTTTCTT 1980
DB 1921 CTGATCACCGTTGAAGAGGTTCCATTGGAGGTTTGGCTCGCAGCTTGTTCAGTTTCTT 1980
QY 1981 GCTCTCGATGCTCTTCTGATGCAAACTCAAGTGGAGACCAATGCTACTGCTGTATGCA 2040
DB 1981 GCTCTCGATGCTCTTCTGATGCAAACTCAAGTGGAGACCAATGCTACTGCTGTATGCA 2040
QY 2041 TACATTGATCACGTGCACACAGCTGATCAACTAGCTGAAGCTGGAATCATGCTCATCTCAC 2100
DB 2041 TACATTGATCACGTGCACACAGCTGATCAACTAGCTGAAGCTGGAATCATGCTCATCTCAC 2100
QY 2101 ATCGCAGCAACCGCCTTAACCTTAATCGGTGACCAAGGAGAGCTCTGTTTGCAGAGTAA 2160
DB 2101 ATCGCAGCAACCGCCTTAACCTTAATCGGTGACCAAGGAGAGCTCTGTTTGCAGAGTAA 2160
QY 2161 GAATCTGTTGGCTTAAACATATGATPACAAACACTCTAAATGCAACCCCAAGGTTTCTTCT 2220
DB 2161 GAATCTGTTGGCTTAAACATATGATPACAAACACTCTAAATGCAACCCCAAGGTTTCTTCT 2220
QY 2221 AGTACTGATCAGAAATCCGCGCGAGAGTCTGTTGGCAACAGCTATATATATTTACTA 2280
DB 2221 AGTACTGATCAGAAATCCGCGCGAGAGTCTGTTGGCAACAGCTATATATATTTACTA 2280
QY 2281 AGATTGTGAAGAGAAAGGCAAAAGGTTGTCGAAAGATTAGTATTATAGATAAAAC 2340
DB 2281 AGATTGTGAAGAGAAAGGCAAAAGGTTGTCGAAAGATTAGTATTATAGATAAAAC 2340
QY 2341 TGGTATTGTTTGTAAATTTTAGGATGATGAGATCGTGTGTGACCAATTAACAT 2400
DB 2341 TGGTATTGTTTGTAAATTTTAGGATGATGAGATCGTGTGTGACCAATTAACAT 2400
QY 2401 CTTGTAAAATCAATTAATCTCTTGTGATCTTCAATAAGCTTGGTGCACAAAAA 2458
DB 2401 CTTGTAAAATCAATTAATCTCTTGTGATCTTCAATAAGCTTGGTGCACAAAAA 2458